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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5-17-95  
Art Unit: 1635 Phone Number: 2- 076 Serial Number: 0914867757  
Location (Bldg/Room#): 2D28 (Mailbox #): 218 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Cytochrome P-450 reductase  
Inventors (please provide full names): KUTCHAN et al.

Earliest Priority Date: 7/13/00

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 10

NA 2649

No Abstract please.

No size limits

Thurs.

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Searcher: \_\_\_\_\_

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 5/20/05

Date Completed: 5/23/05

Searcher Prep & Review Time: \_\_\_\_\_

Online Time: \_\_\_\_\_

Type of Search

/ NA Sequence (#)

AA Sequence (#)

Structure (#)

Bibliographic

Litigation

Fulltext

Other

Vendors and cost where applicable

STN Dialog

Questel/Orbit Lexis/Nexis

Westlaw WWW/Internet

030 In-house sequence systems

Commercial Oligomer Score/Length  
Interference SPDI Encode/Transl  
Other (specify)

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:00:17 ; Search time 8884 Seconds  
(without alignments)  
12172.472 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: 1 cggcagcagcttcttagtat.....tttgagagaaaaaaaaa 2649

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents\_NA\_Main:\*

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116: /cgn2\_6/ptodata/1/pna/US100A45\_COMB.seq.\*

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:22:02 ; Search time 760 Seconds  
(without alignments)  
7754.887 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: 1 cggcagcagctcttagtcat.....tttgagaaaaaaaaaaaa 2649

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 11689648 seqs, 1112441377 residues

Total number of hits satisfying chosen parameters: 23379296

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New:\*

1:	/cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq:*
2:	/cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq2:*
3:	/cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
4:	/cgn2_6/prodata/1/pna/US07_NEW_COMB.seq:*
5:	/cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
6:	/cgn2_6/prodata/1/pna/US09_NEW_COMB.seq:*
7:	/cgn2_6/prodata/1/pna/US10_NEW_COMB.seq:*
8:	/cgn2_6/prodata/1/pna/US10_NEW_COMB.seq2:*
9:	/cgn2_6/prodata/1/pna/US10_NEW_COMB.seq3:*
10:	/cgn2_6/prodata/1/pna/US10_NEW_COMB.seq4:*
11:	/cgn2_6/prodata/1/pna/US11_NEW_COMB.seq:*
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13:	/cgn2_6/prodata/1/pna/US11_NEW_COMB.seq3:*
14:	/cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	Score	Match	Length	nd
No.					

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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 08:25:35 ; Search time 1432 Seconds

(without alignments)  
11343.938 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649  
Sequence: 1 cggcagcagctgtctgtat.....tttggagaaaaa 2649

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 306160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
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- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 04:40:28 ; Search time 455 Seconds  
(without alignments)  
9526.367 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649  
Sequence: 1 cggcagcagcttgtagat.....tttggagaaaaaaaaaaaaa 2649

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_MA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*
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- 4: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 00:44:41 / Search time 1305 Seconds  
(without alignments)  
12016.394 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649  
Sequence: 1 CGGCACGAGCTCTAGTAT.....tttcgagaaaaaaaaaaaaa 2649

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
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3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
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11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 02:29:27 ; Search time 11003 Seconds  
(without alignments)  
11665.715 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctctgttagtat.....tttctggaataaaaaa 2649

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl: 1: gb\_ba: 2: gb\_bhg: 3: gb\_in: 4: gb\_om: 5: gb\_ov: 6: gb\_pac: 7: gb\_ph: 8: gb\_pl: 9: gb\_pr: 10: gb\_ro: 11: gb\_sas: 12: gb\_sy: 13: gb\_un: 14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2645.8	99.9	2650	8	PSU67185
2	1126.4	42.5	2498	8	AF302496 Hybrid po
3	1104.8	41.7	2617	8	VIRNADHP4
4	1094.8	41.3	2641	8	VSNFR
5	1086.2	41.0	2633	8	AY170374
6	1071.4	40.5	2693	8	AB086169
7	1061.4	40.1	2685	8	BT013756
8	1039	39.2	2079	8	AY586976
9	1030.8	38.9	2059	8	AY520902
10	997.2	37.6	2340	8	AY054688
11	994.6	37.5	2079	8	BT008426
12	987.6	37.3	2199	8	ATATR1G
13	985	37.2	2114	6	A75959
14	969.8	36.6	2561	8	ECU67186
15	918.6	34.7	2493	8	AF302497
16	912.6	34.5	2631	8	PM14CPR
17	911.2	34.4	2610	8	AF302498
18	895.4	33.8	2136	6	AX506108
19	895.4	33.8	2136	6	AX651759

20	895.4	33.8	2136	8	AF325101	AF325101 Arabidops
21	875.2	33.0	2556	8	AF024635	AF024635 Petrosell
22	875	33.0	2290	8	ATATR2M	X65017 A.thaliana
23	875	33.0	2423	6	A75961	A75961 Sequence 3
24	874	33.0	2466	8	AF024634	AF024634 Petrosell
25	873.6	33.0	2618	8	CRCRPA	X69791 C.roseus cp
26	867.4	32.7	2333	8	AF123610	AF123610 Trifolium
27	864.8	32.6	2472	8	AY532374	AY532374 Armi maju
28	862.4	32.6	2545	8	AF002698	AF002698 Pisum sat.
29	859.8	32.5	2412	6	A75963	A75963 Sequence 5
30	852.6	32.2	2482	8	AK102060	AK102060 Oryza sat
31	850	32.1	2420	8	TAB303373	AJ303373 Trifolium
32	808.4	30.5	2298	8	AK068915	AK068915 Oryza sat
33	808.4	30.5	2298	8	AK090083	AK090083 Oryza sat
34	807.6	30.5	1863	6	AR205034	AR205034 Sequence
35	807.6	30.5	1863	6	AR282641	AR282641 Sequence
36	807.6	30.5	1863	6	AX082548	AX082548 Sequence
37	807.6	30.5	1863	6	AX370663	AX370663 Sequence
38	807.6	30.5	1863	8	HTU2NFR	226250 H.tuberosus
39	659.2	24.9	1539	8	HTU2NFR	226251 H.tuberosus
40	606.6	22.9	1714	8	AK101320	AK101320 Oryza sat
41	586.4	22.1	2016	6	AK654074	AK654074 Sequence
42	569.6	21.5	2312	8	AF367288	AF367288 Arabidops
43	473.6	17.9	1023	8	AY059162	AY059162 Arabidops
44	295.8	11.2	715	8	HTU58629	U58629 Helianthus
45	282.4	10.7	1078	8	PAB132538	AJ132538 Picea abi

## ALIGNMENTS

RESULT 1  
PSU67185  
LOCUS  
DEFINITION  
PAPAYER SOMNIFERUM NADPH:FERRIHEMOPROTEIN OXIDOREDUCTASE mRNA,  
complete cds.  
ACCESSION  
U67185  
VERSION  
U67185.1 GI:2580496  
KEYWORDS  
SOURCE  
ORGANISM  
Papaver somniferum (opium poppy)  
Papaver somniferum  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
Papaveraceae; Papaver.  
REFERENCE  
1 (bases 1 to 2650)  
Rosco, A., Pauli, H.H., Priemer, W. and Kutchan, T.M.  
Cloning and heterologous expression of NADPH-cytochrome P450  
reductases from the Papaveraceae  
Arch. Biochem. Biophys. 348 (2), 369-377 (1997)  
JOURNAL  
MEDLINE  
9809363  
PUBMED  
9434750  
REFERENCE  
2 (bases 1 to 2650)  
Rosco, A. and Kutchan, T.M.  
Direct Submision  
Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,  
Universitaet Muenchen, Karlstraase 29, Munich 80333, Germany  
FEATURES  
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1..2650  
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NIVISGDLGLYCGKAKMADVHRTIHTTIAOEGCPRESSAALAAVKLOQYERVIAND



